

Figure 1
Interleukin-21

1 GGCACGAGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCT 60
1 A R V D T D E D R Y P Q K L A F A E C L 20
Domain I Domain II

61 GTGCAGAGGCTGTATCGATGCACGGACGGGCGCGAGACAGCTGGCCTCAACTCCGTGCG 120
21 C R G C I D A R T G R E T A A L N S V R 40
Domain II

121 GCTGCTCCAGAGCCTGCTGGTGTGCTGCGCCGCGGCCCTGCTCCCGCGACGGCTCGGGGCT 180
41 L L Q S L L V L R R R P C S R D G S G L 60
Domain III

181 CCCACACCTGGGGCCTTTGCCTTCCACACGAGTTTCATCCACGTCCCCGTGGGCTGCAC 240
61 P T P G A F A F H T E F I H V P V G C T 80
Domain IV

241 CTGCGTGTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACACGT 300
81 C V L P R S V 87
Domain IV

301 GTGCTCCCCAGAGGGCACCCCCCTATTTATGTATTATTATTATTATATGCTCCCCC 360

361 AACACTACCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTC 420

421 CTCATCTCCAGCCTCAGTAGTTGGGGGTGGAAGGAGCTCAGCACCTCTTCCAGCCCTTAA 480

481 AGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGYTCCCTGTCTGCTCCCGCT 540

541 TCCCTTACCTTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGA 600

601 AGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACAC 660

661 AA 705

000021 " STEE 60

Figure 2A
Interleukin-22

1 GGAATTCGGCACGAGCTCGTGCCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGC 60
1 N S A R A R A V L S A F H H T L Q L G P 20

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61 CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCGACCGCCGCT 120
21 R E Q A R N A S C P A G G R P A D R R F 40

121 TCCGCGCGCCACCAACCTGCGCAGCGTGTGCGCCTGGGCCTACAGAATCTCCTACGACC 180
41 R P P T N L R S V S P W A Y R I S Y D P 60
Domain I

181 CGGCGAGGTACCCCAAGTACCTGCCTGAAGCCTACTGCCTGTGCGGGGCTGCCTGACCG 240
61 A R Y P R Y L P E A Y C L C R G C L T G 80
Domain I Domain II

241 GGCTGTTCCGCGAGGAGGACGTGCGCTTCCGCGAGCGCCCTGTCTACATGCCACCGTCG 300
81 L F G E E D V R F R S A P V Y M P T V V 100
Domain III

301 TCCTGCGCCGCACCCCGCCTGCGCGGGCGCGCGTTCCGTCTACACCGAGGCCTACGTCA 360
101 L R R T P A C A G G R S V Y T E A Y V T 120
Domain III

#

361 CCATCCCCGTGGGCTGCACCTGCGTCCCCGAGCGGAGAAGGACGACAGCATCAACT 420
121 I P V G C T C V P E P E K D A D S I N S 140
Domain IV

421 CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCGCTGGCC 480
141 S I D K Q G A K L L L G P N D A P A G P 160

481 CCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGGCCCGCATCCCGAGGCGCCCAAGCTG 540

541 GAGCCGCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGACCGAGCAAACCAAGTG 600

601 CCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCA 660

661 TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC 720

721 CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCC 780

781 CTGAGGAGCCTCTCAGATCGGCTGCTGCGGGTGCAGGGCGTGACTCACCGCTGGGTGCTT 840

841 GCCAAAGAGATAGGGACGCATATGCTTTTAAAGCAATCTAAAAATAATAATAAGTATAG 900

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Figure 2B
Interleukin-22

901 CGACTATATACCTACTTTTAAATCAACTGTTTGAATAGAGGCAGAGCTATTTTATATT 960
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC 1020
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTGTAGCTGGTACACTC 1080
1081 TGGCCTGGGCTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCT 1140
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCTCCAGGTGGACCAAAGGG 1200
1201 ATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTGG 1260
1261 TTTTAGTCATGAATACATAAACAGTCTCAAAGTGCACAATTTTTTCCCCCTTTTGAAAG 1320
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGAACGTGACATCTTT 1380
1381 GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440
1441 CTGAATATGAGGACAAAGTGGGCCAGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500
1501 GTTCTGCAATCTGCCACGAGAGCTAGGTCCCTGATCTTTCTTTAGATTGAAAGTCTGT 1560
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTCTTTTAAATCATTAAAAGAGGCTT 1620
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642

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D-216 III

	10	20	30	40	50
1	M T P G K T S L V S L	- - L L L L S L	- E A I V K A G I T I P R N P G C P N S E D	- - - -	II-17.aa
1	M S P G R A S V S L M L	- - L L L L S L	- A A T V K A A A I I P Q S S A C P N T E A	- - - -	mII-17.aa
1	M T F R M T S L V - L	- - L L L L S I	- D C I V K S E I T S A Q T P R C L A A N N	- - - -	vII-17.aa
1	M D W P H N L L F L L	T I S I F L G L G Q P R S P K S K R K G Q G R P G P L A P G P H Q V P L D L V	- - - -	- - - -	II-20.aa
1	A - - - - -	- - - - -	- - - - -	- - - - -	II-21.aa
1	M T L L P G L L F L - -	- T W L H T C L A H H D P S L R G H P H S H G T P H C Y S A E E L P L G Q A	- - - - -	- - - - -	II-21FL.aa
1	- - - - -	- - - - - N S A R - - - - -	- - - - -	- - - - -	II-22.aa
1	- - - - -	- - - - - G C A D R P E E L L E - - - - -	- - - - -	- - - - -	II-22ex.aa

	60	70	80	90	100	
39	-	-	-	-	-	IL-17.aa
41	-	-	-	-	-	mIL-17.aa
38	-	-	-	-	-	vIL-17.aa
51	S R M K P Y A R M E E Y E R N I E - E M V A Q L R N S S E L A Q R - - - - K C E V - - - - N					II20.aa
2	-	-	-	-	-	IL-21.aa
48	P P - H L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T Q C P V L - R P E E					II21FL.aa
5	-	-	-	-	-	IL-22.aa
12	-	-	-	-	-	II22ext.aa

Figure 3A

	110	120	130	140	150	
67	- - - - - Y	N R S T S P W N L H R N E D P E R Y P S V I W E A K C R H L G C I N A D - G N V D Y	IL-17.aa			
70	- - - - - L	N R S T S P W T L H R N E D P D R Y P S V I W E A Q C R H Q R C V N A E - G K L D H	mIL-17.aa			
63	- - - - - Y	N R S T S P W T L H R N E D Q D R Y P S V I W E A K C R Y L G C V N A D - G N V D Y	vIL-17.aa			
88	L Q L W M S N K - R S L S P W G Y S I N H D P S R I P V D L P E A R C L C L G C V N P F T M Q E D R	IL20.aa				
2	- - - - -	- - - - - R V D T D E D R Y P Q K L A F A E C L C R G C I D A R T G R E T A	IL-21.aa			
96	V - L E A D T H Q R S I S P W R Y R V D T D E D R Y P Q K L A F A E C L C R G C I D A R T G R E T A	IL21FL.aa				
38	R R F R P P T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C L T G L F G E E D V	IL-22.aa				
1	R R F R P P T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C L T G L F G E E D V	IL22ext				

	160	170	180	190	200	
109	H M N S V P I Q Q E I L V L R R E P - - - - - P H C P N S F R L E K I L - - V S V G C T C V T P I L-17.aa					
112	H M N S V L I Q Q E I L V L K R E P - - - - - E S C P F T F R V E K M L - - V G V G C T C V A S mIL-17.aa					
105	H M N S V P I Q Q E I L V V R K G H - - - - - Q P C P N S F R L E K M L - - V T V G C T C V T P vIL-17.aa					
137	S M V S V P V F - S Q V P V R R R L C P P P R T G P C R Q - - - R A V M E T I A V G C T C I - - I L20.aa					
35	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - I L-21.aa					
145	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - I L21FL.aa					
88	R F R S A P V Y M P T V L R R T P A C A G G R S V - - - - - Y T E A Y V T I P V G C T C V P E I L-22.aa					
101	R F R S A P V Y M P T V L R R T P A C A G G R S V - - - - - Y T E A Y V T I P V G C T C V P E I L22ext.aa					

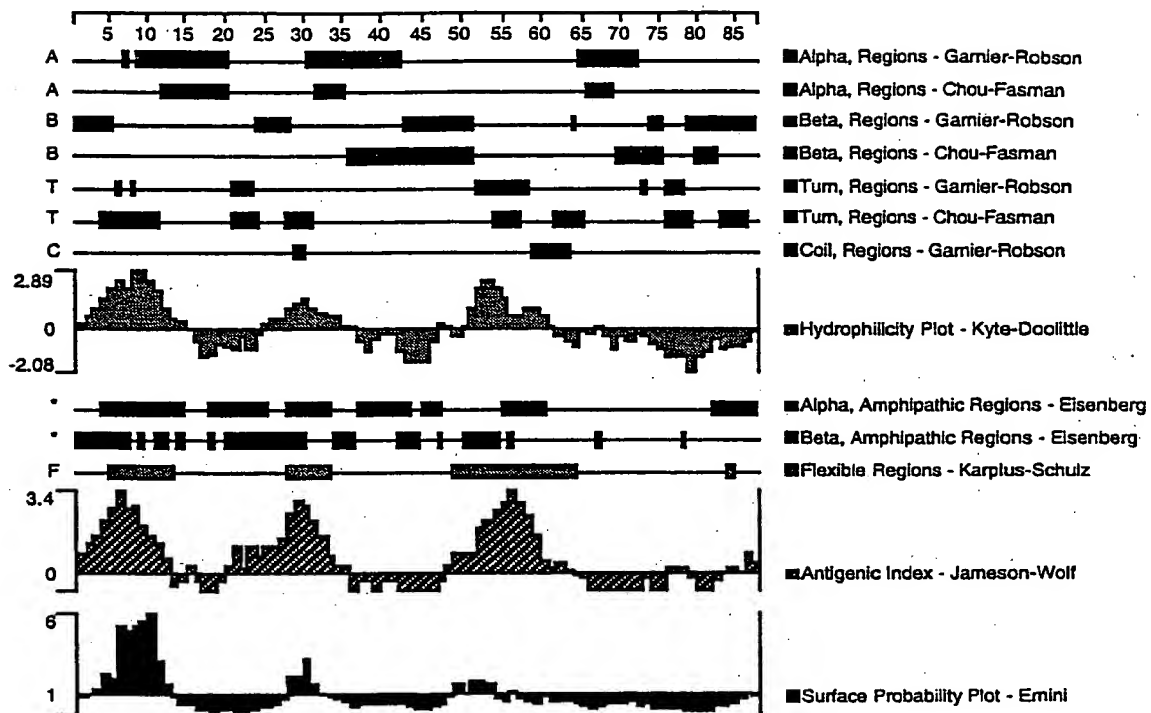
Figure 3B

	210	220	230
150	I V H H V A		
153	I V R Q A A		
146	I V H N V D		
180	- - - - -	- - - - -	- - - F
83	- - - - -	- - - - -	- L P R S V
193	- - - - -	- - - - -	- L P R S V
131	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P		
44	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P		

IL-17.aa
mIL-17.aa
vIL-17.aa
IL20.aa
IL-21.aa
IL21FL.aa
IL-22.aa
IL22ext

Figure 3C

Figure 4
Interleukin-21 Polypeptide Analysis



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0-9 **A** **B** **C** **D** **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

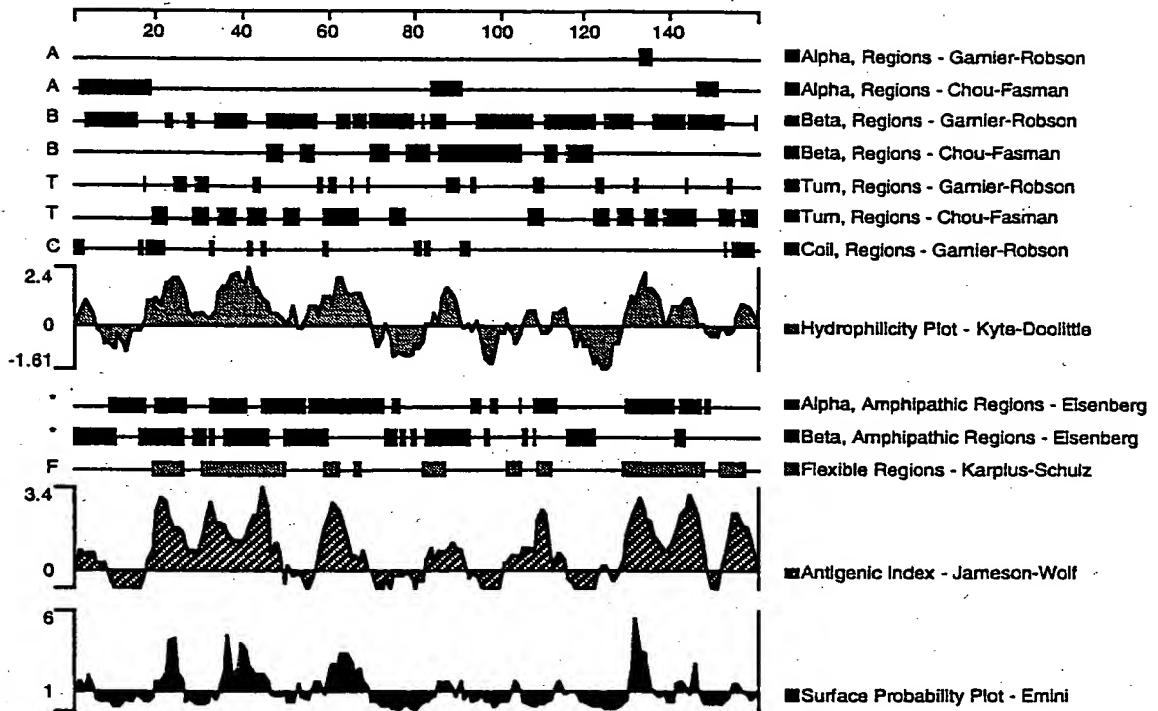


Figure 6A
Interleukin-21

1 GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCGGCCCTCCTGTTT 60
1 M T L L P G L L F 9

61 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCAGCCCCAC 120
10 L T W L H T C L A H H D P S L R G H P H 29

121 AGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTCCCCCTCGGCCAGGCCCCCCCA 180
30 S H G T P H C Y S A E E L P L G Q A P P 49
Domain V

181 CACCTGCTGGCTCGAGGTGCCAAGTGGGGGAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 240
50 H L L A R G A K W G Q A L P V A L V S S 69
Domain VI

241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG 300
70 L E A A S H R G R H E R P S A T T Q C P 89

301 GTGCTGGGCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGG 360
90 V L R P E E V L E A D T H Q R S I S P W 109
Domain VII

361 AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 420
110 R Y R V D T D E D R Y P Q K L A F A E C 129
Domain I Domain II

421 CTGTGCAGAGGCTGTATCGATGCACGGACGGGCGCGAGACAGCTGCGCTCAACTCCGTG 480
130 L C R G C I D A R T G R E T A A L N S V 149
Domain II

481 CGGCTGCTCCAGAGCCTGCTGGTGTGCGCGCGCGGCCCTGCTCCCGCGACGGCTCGGGG 540
150 R L L Q S L L V L R R R P C S R D G S G 169
Domain III

541 CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTTCATCCACGTCCCGCTCGGCTGC 600
170 L P T P G A F A F H T E F I H V P V G C 189
Domain IV

601 ACCTGCGTGCTGCCCCGTTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC 660
190 T C V L P R S V 197
Domain IV

661 GTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 720

721 CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTC 780

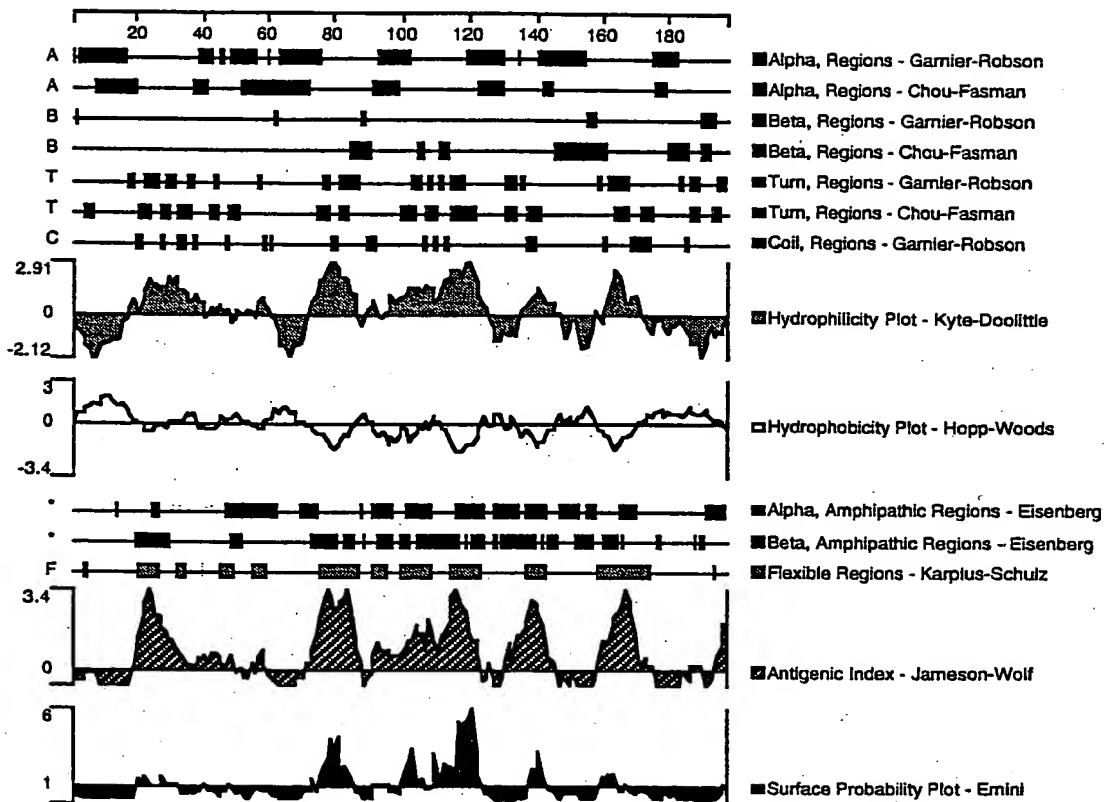
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Figure 6B
Interleukin-21

781 TCCTCATCTCCAGCCTCAGTAGTTGGGGTGAAGGAGCTCAGCACCTCTTCCAGCCCTT 840
841 AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCTCTGCTCCCGG 900
901 CTTCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960
961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTATTATTAAACTGATGAAC 1020
1021 AA 1067

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Figure 7
Interleukin-21 Polypeptide Analysis



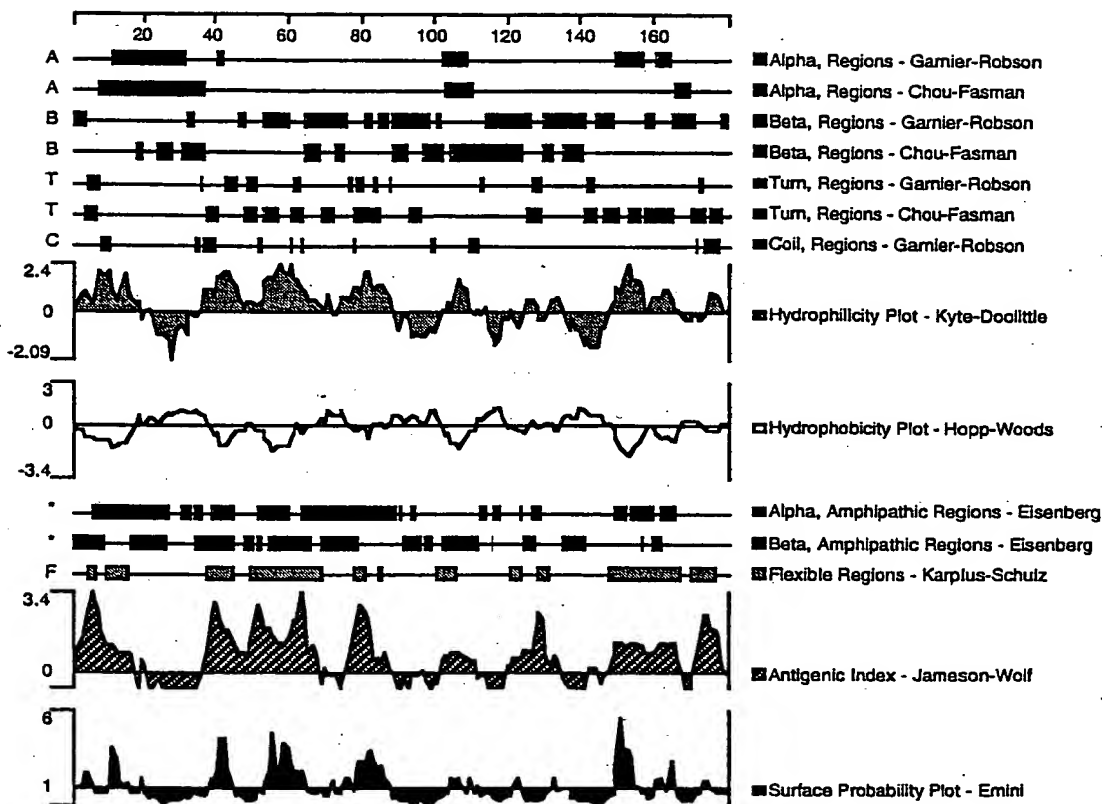
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Figure 8
Interleukin-22

1	GGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGCG	60
1	G C A D R P E E L L E Q L Y G R L A A G	20
	CD-VI	
61	GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCG	120
21	<u>V L S A F H H T L Q L G P R E Q A R N A</u>	40
	CD-VI	
121	AGCTGCCCCGCGAGGGGGCAGGCCCGCGACCGCGCTTCCGGCCGCCCACCAACCTGCGC	180
41	S C P A G G R P A D R R F R P P T N L R	60
181	AGCGTGTGCCCCCTGGGCCTACAGAATCTCCTACGACCCGCGAGGTACCCCAGGTACCTG	240
61	<u>S V S P W A Y R I S Y D P A R Y P R Y L</u>	80
	CD-VII	CD-I
241	CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCCGGCGAGGAGGACGTG	300
81	P E A Y C L C R G C L T G L F G E E D V	100
	CD-II	
301	CGCTTCCGCAGCGCCCCCTGTCTACATGCCCACCGTCGTCTGCGCCGCACCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P A C</u>	120
	CD-III	
361	GCCGGCGGCGGTTCCGTCTACACCGAGGCCTACGTACCATCCCCGTGGGCTGCACCTGC	420
121	A G G R S V Y T E A Y V T <u>I P V G C T C</u>	140
	CD-IV	
421	GTCCCCGAGCCGAGAGAAGGACGCGAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V P E P E K D A D S I N S S I D K Q G A</u>	160
	CD-IV	
481	AAGTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGA	522
161	K L L L G P N D A P A G P	174

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Figure 9
Interleukin-22 Polypeptide Analysis



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